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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/754,014

DATE: 01/23/2002

TIME: 14:37:02

Input Set : N:\Crf3\RULE60\09754014.raw

Output Set: N:\CRF3\01232002\I754014.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Jeff Nordstrom

7 Bruce Freimark

8 Deepa Deshpande

11 (ii) TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS

12 AND USES

15 (iii) NUMBER OF SEQUENCES: 12

18 (iv) CORRESPONDENCE ADDRESS:

20 (A) ADDRESSEE: Lyon &amp; Lyon

21 (B) STREET: 633 West Fifth Street

22 Suite 4700

23 (C) CITY: Los Angeles

24 (D) STATE: California

25 (E) COUNTRY: U.S.A.

26 (F) ZIP: 90071-2066

29 (v) COMPUTER READABLE FORM:

31 (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

32 storage

33 (B) COMPUTER: IBM Compatible

34 (C) OPERATING SYSTEM: IBM P.C. DOS 5.0

35 (D) SOFTWARE: FastSEQ for Windows 2.0

38 (vi) CURRENT APPLICATION DATA:

C--&gt; 40 (A) APPLICATION NUMBER: US/09/754,014

C--&gt; 41 (B) FILING DATE: 03-Jan-2001

42 (C) CLASSIFICATION:

45 (vii) PRIOR APPLICATION DATA:

47 (A) APPLICATION NUMBER: 08/948,958

48 (B) FILING DATE:

51 (viii) ATTORNEY/AGENT INFORMATION:

53 (A) NAME: Berkman, Charles S.

54 (B) REGISTRATION NUMBER: 38,077

55 (C) REFERENCE/DOCKET NUMBER: 226/284

57 (ix) TELECOMMUNICATION INFORMATION:

59 (A) TELEPHONE: (213) 489-1600

60 (B) TELEFAX: (213) 955-0440

61 (C) TELEX: 67-3510

69 (2) INFORMATION FOR SEQ ID NO: 1:

71 (i) SEQUENCE CHARACTERISTICS:

73 (A) LENGTH: 328 amino acids

74 (B) TYPE: amino acid

75 (C) STRANDEDNESS: single

76 (D) TOPOLOGY: linear

ENTERED

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```

78      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
80  Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu
81      1          5          10          15
83  Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
84          20          25          30
86  Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
87          35          40          45
89  Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln
90          50          55          60
92  Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
93      65          70          75          80
95  Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
96          85          90          95
98  Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
99          100         105         110
101  Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
102          115         120         125
104  Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
105          130         135         140
107  Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg
108          145         150         155         160
110  Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
111          165         170         175
113  Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
114          180         185         190
116  Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
117          195         200         205
119  Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
120          210         215         220
122  Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
123          225         230         235         240
125  Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
126          245         250         255
128  Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
129          260         265         270
131  Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
132          275         280         285
134  Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
135          290         295         300
137  Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
138          305         310         315         320
141  Glu Trp Ala Ser Val Pro Cys Ser
142          325

```

146 (2) INFORMATION FOR SEQ ID NO: 2:

148 (i) SEQUENCE CHARACTERISTICS:

150 (A) LENGTH: 987 base pairs

151 (B) TYPE: nucleic acid

152 (C) STRANDEDNESS: single

153 (D) TOPOLOGY: linear

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155 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

157	ATGTGTCACC	AGCAGTTGGT	CATCTCTTGG	TTTTCCCTGG	TTTTTCTGGC	ATCTCCCTC	60
158	GTGGCCATAT	GGGAAGTAA	GAAAGATGTT	TATGTCGTAG	AATTGGATTG	GTATCCGGAT	120
159	GCCCCCTGGAG	AAATGGTGGT	CCTCACCTGT	GACACCCCTG	AAGAAGATGG	TATCACCTGG	180
160	ACCTTGGACC	AGAGCAGTGA	GGTCTTAGGC	TCTGGCAAAA	CCCTGACCAT	CCAAGTCAAA	240
161	GAGTTTGGAG	ATGCTGGCCA	GTACACCTGT	CACAAAGGAG	GCGAGGTCT	AAGCCATTCTG	300
162	CTCCTGCTGC	TTACAAAAA	GGAAGATGGA	ATTTGGTCCA	CTGATATTTT	AAAGGACCAG	360
163	AAAGAACCCA	AAAATAAGAC	CTTTCTAAGA	TGCGAGGCCA	AGAATTATTC	TGGACGTTTC	420
164	ACCTGCTGGT	GGCTGACGAC	AATCAGTACT	GATTTGACAT	TCAGTGTCAA	AAGCAGCAGA	480
165	GGCTCTTCTG	ACCCCCAAGG	GGTGACGTGC	GGAGCTGCTA	CACTCTCTGC	AGAGAGAGTC	540
166	AGAGGGGACA	ACAAGGAGTA	TGAGTACTCA	GTGGAGTGCC	AGGAGGACAG	TGCCTGCCCA	600
167	GCTGCTGAGG	AGAGTCTGCC	CATTGAGGTC	ATGGTGGATG	CCGTTCACAA	GCTCAAGTAT	660
168	GAAACTACA	CCAGCAGCTT	CTTCATCAGG	GACATCATCA	AACCTGACCC	ACCCAAGAAC	720
169	TTGCAGCTGA	AGCCATTAAA	GAATTCTCGG	CAGGTGGAGG	TCAGCTGGGA	GTACCCTGAC	780
170	ACCTGGAGTA	CTCCACATTC	CTACTTCTCC	CTGACATTCT	GCGTTCAGGT	CCAGGGCAAG	840
171	AGCAAGAGAG	AAAAGAAAGA	TAGAGTCTTC	ACGGACAAGA	CCTCAGCCAC	GGTCATCTGC	900
172	CGCAAAAATG	CCAGCATTAG	CGTGCGGGCC	CAGGACCGCT	ACTATAGCTC	ATCTTGGAGC	960
173	GAATGGGCAT	CTGTGCCCTG	CAGTTAG				987

177 (2) INFORMATION FOR SEQ ID NO: 3:

179 (i) SEQUENCE CHARACTERISTICS:

181 (A) LENGTH: 987 base pairs

182 (B) TYPE: nucleic acid

183 (C) STRANDEDNESS: single

184 (D) TOPOLOGY: linear

186 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

188	ATGTGCCACC	AGCAGCTGGT	GATCAGCTGG	TTGAGCCTGG	TGTTCTTGGC	CAGCCCCCTG	60
189	GTGGCCATCT	GGGAGCTGAA	GAAGGACGTG	TACGTGGTGG	AGCTGGACTG	GTACCCCGAC	120
190	GCCCCCGGCG	AGATGGTGGT	GCTGACCTGC	GACACCCCGG	AGGAGGACGG	CATCACCTGG	180
191	ACCCTGGACC	AGAGCAGCGA	GGTGTGGGGC	AGCGGCAAGA	CCCTGACCAT	CCAGGTGAAG	240
192	GAGTTCGGCG	ACGCCGGCCA	GTACACCTGC	CACAAGGGCG	GCGAGGTGCT	GAGCCACAGC	300
193	CTGCTGCTGC	TGCACAAGAA	GGAGGACGGC	ATCTGGAGCA	CCGACATCCT	GAAGGACCAG	360
194	AAGGAGCCCA	AGAACAAGAC	CTTCTGCGC	TGCGAGGCCA	AGAACTACAG	CGGCCGCTTC	420
195	ACCTGCTGGT	GGCTGACCAC	CATCAGCACC	GACCTGACCT	TCAGCGTGAA	GAGCAGCAGG	480
196	GGCAGCAGCG	ACCCCCAGGG	CGTGACCTGC	GGCGCCGCCA	CCCTGAGCGC	CGAGCGCGTG	540
197	CGCGGCGACA	ACAAGGAGTA	CGAGTACAGC	GTGGAGTGCC	AGGAGGACAG	CGCCTGCCCC	600
198	GCCGCCGAGG	AGAGCCTGCC	CATCGAGGTG	ATGGTGGACG	CCGTCCACAA	GCTGAAGTAC	660
199	GAGAACTACA	CCAGCAGCTT	CTTCATCCGC	GACATCATCA	AGCCCGACCC	CCCCAAGAAC	720
200	CTGCAGCTGA	AGCCCCTGAA	GAACAGCCGC	CAGGTGGAGG	TGAGCTGGGA	GTACCCCGAC	780
201	ACCTGGAGCA	CCCCCACAG	CTACTTCAGC	CTGACCTTCT	GCGTGCAGGT	GCAGGGCAAG	840
202	AGCAAGCGCG	AGAAGAAGGA	CCGCGTGTTT	ACCGACAAGA	CCAGCGCCAC	CGTGATCTGC	900
203	CGCAAGAACG	CCAGCATCAG	CGTGCGCGCC	CAGGACCGCT	ACTACAGCAG	CAGCTGGAGC	960
204	GAGTGGGCCA	GCGTGCCCTG	CAGCTAG				987

206 (2) INFORMATION FOR SEQ ID NO: 4:

208 (i) SEQUENCE CHARACTERISTICS:

210 (A) LENGTH: 987 base pairs

211 (B) TYPE: nucleic acid

212 (C) STRANDEDNESS: single

213 (D) TOPOLOGY: linear

215 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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217 ATGTGCCACC AGCAGCTGGT GATCAGCTGG TTCTCCCTGG TGTTCCTGGC CAGCCCCCTC 60
218 GTGGCCATCT GGGAGCTGAA GAAAGACGTG TACGTGGTCG AGCTGGACTG GTACCCCGAC 120
219 GCCCCCGGCG AGATGGTGGT CCTGACCTGC GACACCCCGG AGGAAGACGG CATCACCTGG 180
220 ACCCTGGACC AGAGCAGTGA GGTGCTGGGC TCCGGCAAGA CCCTGACCAT CCAGGTGAAG 240
221 GAGTTCGGCG ACGCCGGCCA GTACACCTGC CACAAGGGAG GCGAGGTGCT GAGCCACTCC 300
222 CTCCTGCTGC TCCACAAAAA GGAGGACGGC ATCTGGAGCA CCGACATCCT GAAGGACCAG 360
223 AAGGAGCCCA AGAACAAGAC CTTCTGCGC TGCAGGCCA AGAACTACAG CGGCCGCTTC 420
224 ACCTGCTGGT GGCTGACCAC GATCAGCACC GACCTGACCT TCAGTGTGAA GAGCAGCAGG 480
225 GGCTCCAGCG ACCCCCAGGG CGTGACCTGC GCGCTGCCA CCCTGAGCGC CGAGCGCGTG 540
226 CGCGGCGACA ACAAGGAGTA CGAGTACAGC GTGGAGTGCC AGGAAGACTC CGCCTGCCCC 600
227 GCCGTGAGG AGAGCCTGCC CATCGAGGTG ATGGTGACG CCGTTCACAA GCTGAAGTAC 660
228 GAGAACTACA CCAGCAGCTT CTTATCCGC GACATCATCA AGCCTGACCC ACCCAAGAAC 720
229 CTCCAGCTGA AGCCCCCAA GAACTCCGC CAGGTGGAGG TGAGCTGGGA GTACCCCGAC 780
230 ACCTGGAGCA CGCCCCACTC CTACTTCTCC CTGACCTTCT GCGTGCAGGT CCAGGGCAAG 840
231 AGCAAGCGCG AGAAGAAAGA CCGGGTGTTT ACCGACAAGA CCAGCGCCAC CGTCATCTGC 900
232 CGCAAGAACG CCAGCATCAG CGTGCGCGCC CAGGACCGCT ACTATAGCTC CTCTTGAGC 960
233 GAGTGGGCCA GCGTGCCCTG CTCCTAG 987

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237 (2) INFORMATION FOR SEQ ID NO: 5:

239 (i) SEQUENCE CHARACTERISTICS:

241 (A) LENGTH: 219 amino acids

242 (B) TYPE: amino acid

243 (C) STRANDEDNESS: single

244 (D) TOPOLOGY: linear

246 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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248 Met Cys Pro Ala Arg Ser Leu Leu Leu Val Ala Thr Leu Val Leu Leu
249 1 5 10 15
251 Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Asp Pro
252 20 25 30
254 Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val
255 35 40 45
257 Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys
258 50 55 60
260 Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
261 65 70 75 80
263 Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys
264 85 90 95
266 Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala
267 100 105 110
269 Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr
270 115 120 125
272 Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys
273 130 135 140
274 Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
275 145 150 155 160
277 Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr
278 165 170 175
280 Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
281 180 185 190
283 Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr

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284          195          200          205
286 Ile Asp Arg Val Thr Ser Tyr Leu Asn Ala Ser
287      210          215
291 (2) INFORMATION FOR SEQ ID NO: 6:
293     (i) SEQUENCE CHARACTERISTICS:
295         (A) LENGTH: 660 base pairs
296         (B) TYPE: nucleic acid
297         (C) STRANDEDNESS: single
298         (D) TOPOLOGY: linear
300     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
302 ATGTGTCCAG CGCGCAGCCT CCTCCTTG TG GCTACCCTGG TCCTCCTGGA CCACCTCACT      60
303 TTGGCCAGAA ACCTCCCCGT GGCCACTCCA GACCCAGGAA TGTTCCCATG CCTTCACCAC      120
304 TCCCAAAACC TGCTGAGGGC CGTCAGCAAC ATGCTCCAGA AGGCCAGACA AACTCTAGAA      180
305 TTTTACCCTT GCACTTCTGA AGAGATTGAT CATGAAGATA TCACAAAAGA TAAAACCAGC      240
306 ACAGTGGAGG CCTGTTTACC ATTGGAATTA ACCAAGAATG AGAGTTGCCT AAATTCCAGA      300
307 GAGACCTCTT TCATAACTAA TGGGAGTTGC CTGGCCTCCA GAAAGACCTC TTTTATGATG      360
308 GCCCTGTGCC TTAGTAGTAT TTATGAAGAC TTGAAGATGT ACCAGGTGGA GTTCAAGACC      420
309 ATGAATGCAA AGCTTCTGAT GGATCCTAAG AGGCAGATCT TTCTAGATCA AAACATGCTG      480
310 GCAGTTATTG ATGAGCTGAT GCAGGCCCTG AATTTCACA GTGAGACTGT GCCACAAAAA      540
311 TCCTCCCTTG AAGAACCGGA TTTTATAAA ACTAAAATCA AGCTCTGCAT ACTTCTTCAT      600
312 GCTTTCAGAA TTCGGGCAGT GACTATTGAC AGAGTGACGA GCTATCTGAA TGCTTCCTAA      660
316 (2) INFORMATION FOR SEQ ID NO: 7:
318     (i) SEQUENCE CHARACTERISTICS:
320         (A) LENGTH: 660 base pairs
321         (B) TYPE: nucleic acid
322         (C) STRANDEDNESS: single
323         (D) TOPOLOGY: linear
325     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
327 ATGTGCCCCG CCCGCGCAGCCT GCTGCTGGTG GCCACCCTGG TGCTGCTGGA CCACCTGAGC      60
328 CTGGCCCCGA ACCTGCCCCGT GGCCACCCCC GACCCCGGCA TGTTCCCCTG CCTGCACCAC      120
329 AGCCAGAACC TGCTGGCGGC CGTGAGCAAC ATGCTGCAGA AGGCCGCGCA GACCCTGGAG      180
330 TTCTACCCCT GCACCAGCGA GGAGATCGAC CACGAGGACA TCACCAAGGA CAAGACCAGC      240
331 ACCGTGGAGG CCTGCCTGCC CCTGGAGCTG ACCAAGAACG AGAGCTGCCT GAACAGCCGC      300
332 GAGACCAGCT TCATACCAA CGGCAGCTGC CTGGCCAGCC GCAAGACCAG CTTTCATGATG      360
333 GCCCTGTGCC TGAGCAGCAT CTACGAGGAC CTGAAGATGT ACCAGGTGGA GTTCAAGACC      420
334 ATGAACGCCA AGCTGCTGAT GGACCCCAAG CTCCAGATCT TCCTGGACCA GAACATGCTG      480
335 GCCGTGATCG ACGAGCTGAT GCAGGCCCTG AACTTCAACA GCGAGACCGT GCCCCAGAAG      540
336 AGCAGCCTGG AGGAGCCCGA CTTCTACAAG ACCAAGATCA AGCTGTGCAT CCTGCTGCAC      600
337 GCCTTCCGCA TCCGCGCCGT GACCATCGAC CGCGTGACCA GCTACCTGAA CGCCACCTGA      660
342 (2) INFORMATION FOR SEQ ID NO: 8:
344     (i) SEQUENCE CHARACTERISTICS:
346         (A) LENGTH: 660 base pairs
347         (B) TYPE: nucleic acid
348         (C) STRANDEDNESS: single
349         (D) TOPOLOGY: linear
351     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
353 ATGTGCCCCG CCCGCGCAGCCT GCTGCTCGTG GCCACCCTGG TGCTCCTGGA CCACCTCAGC      60
354 CTGGCCCCGA ACCTCCCCGT GGCCACCCCA GACCCCGGCA TGTTCCCATG CCTGCACCAC      120
355 AGCCAGAACC TGCTGGCGGC CGTGAGCAAC ATGCTGCAGA AGGCCGCGCA GACCCTGGAG      180

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VERIFICATION SUMMARY

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DATE: 01/23/2002

TIME: 14:37:03

Input Set : N:\Crf3\RULE60\09754014.raw

Output Set: N:\CRF3\01232002\I754014.raw

L:40 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:41 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]